#11

1632   1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/729,658C

DATE: 08/06/2002
TIME: 17:02:16

Input Set : A:\55924.app
Output Set: N:\CRF3\08062002\I729658C.raw

P.6

```
 3 <110> APPLICANT: Zonana et al.
 5 <120> TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
 7 <130> FILE REFERENCE: 55924
 9 <140> CURRENT APPLICATION NUMBER: 09/729,658C
10 <141> CURRENT FILING DATE: 2000-12-04
12 <150> PRIOR APPLICATION NUMBER: 09/342,681
13 <151> PRIOR FILING DATE: 1999-06-29
15 <150> PRIOR APPLICATION NUMBER: 60/092,279
16 <151> PRIOR FILING DATE: 1998-07-09
18 <150> PRIOR APPLICATION NUMBER: 60/112,366
19 <151> PRIOR FILING DATE: 1998-12-15
21 <160> NUMBER OF SEQ ID NOS: 127
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1574
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (242)..(1417)
34 <400> SEQUENCE: 1
35 attccctcgg cgggccagcc tcccctctct cccgcccctc ctcctccctt tcccacccct 60
37 cggagtagag ctgcacatgc ggctgctccc tgctccgtcc cgcccagcca ctgtcgcgca 120
39 ggaacgggtc cctgcagccc ccagccgatg gcaggacagt agccgcctgt cagaggtcgt 180
41 gaacggctga ggcagacgca gcggctcccg ggcctcaaga gagtgggtgt ctccggaggc 240
43 c atg ggc tac ccg gag gtg gag cgc agg gaa ctc ctg cct gca gca gcg 289
44   Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala
45    1               5                  10                  15
47 ccg cgg gag cga ggg agc cag ggc tgc ggg tgt ggc ggg gcc cct gcc 337
48 Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
49             20                  25                  30
51 cgg gcg ggc gaa ggg aac agc tgc ctg ctc ttc ctg ggt ttc ttt ggc 385
52 Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
53         35                  40                  45
55 ctc tcg ctg gcc ctc cac ctg ctg acg ttg tgc tgc tac cta gag ttg 433
56 Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
57     50                  55                  60
59 cgc tcg gag ttg cgg cgg gaa cgt gga gcc gag tcc cgc ctt ggc ggc 481
60 Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
61 65                  70                  75                  80
63 tcg ggc acc cct ggc acc tct ggc acc cta agc agc ctc ggt ggc ctc 529
64 Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
65                  85                  90                  95
```

```
 67 gac cct gac agc ccc atc acc agt cac ctt ggg cag ccg tca cct aag   577
 68 Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
 69             100                 105                 110
 71 cag cag cca ttg gaa ccg gga gaa gcc gca ctc cac tct gac tcc cag   625
 72 Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
 73         115                 120                 125
 75 gac ggg cac cag atg gcc cta ttg aat ttc ttc ttc cct gat gaa aag   673
 76 Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
 77         130                 135                 140
 79 cca tac tct gaa gaa gaa agt agg cgt gtt cgc cgc aat aaa aga agc   721
 80 Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
 81 145                 150                 155                 160
 83 aaa agc aat gaa gga gca gat ggc cca gtt aaa aac aag aaa aag gga   769
 84 Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
 85             165                 170                 175
 87 aag aaa gca gga cct cct gga ccc aat ggc cct cca gga ccc cca gga   817
 88 Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
 89         180                 185                 190
 91 cct cca gga ccc cag gga ccc cca gga att cca ggg att cct gga att   865
 92 Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
 93         195                 200                 205
 95 cca gga aca act gtt atg gga cca cct ggt cct cca ggt cct cct ggt   913
 96 Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
 97         210                 215                 220
 99 cct caa gga ccc cct ggc ctc cag gga cct tct ggt gct gct gat aaa   961
100 Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
101 225                 230                 235                 240
103 gct gga act cga gaa aac cag cca gct gtg gtg cat cta cag ggc caa  1009
104 Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
105                 245                 250                 255
107 ggg tca gca att caa gtc aag aat gat ctt tca ggt gga gtg ctc aat  1057
108 Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
109         260                 265                 270
111 gac tgg tct cgc atc act atg aac ccc aag gtg ttt aag cta cat ccc  1105
112 Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
113         275                 280                 285
115 cgc agc ggg gag ctg gag gta ctg gtg gac ggc acc tac ttc atc tat  1153
116 Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
117         290                 295                 300
119 agt cag gta gaa gta tac tac atc aac ttc act gac ttt gcc agc tat  1201
120 Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
121 305                 310                 315                 320
123 gag gtg gtg gtg gat gag aag ccc ttc ctg cag tgc aca cgc agc atc  1249
124 Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
125                 325                 330                 335
127 gag acg ggc aag acc aac tac aac act tgc tat acc gca ggc gtc tgc  1297
128 Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
129         340                 345                 350
131 ctc ctc aag gcc cgg cag aag atc gcc gtc aag atg gtg cac gct gac  1345
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/729,658C

DATE: 08/06/2002
TIME: 17:02:16

Input Set : A:\55924.app
Output Set: N:\CRF3\08062002\I729658C.raw

```
132 Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
133     355                   360                   365
135 atc tcc atc aac atg agc aag cac acc acg ttc ttt ggg gcc atc agg      1393
136 Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
137     370                   375                   380
139 ctg ggt gaa gcc cct gca tcc tag attccccat tttgcctctg tccgtgcccc      1447
140 Leu Gly Glu Ala Pro Ala Ser
141 385                   390
143 ttccctgggt ttgggagcca ggactcccaa aacctctaag tgctgctgtg gagtgaggtg      1507
145 tattggtgtt gcagccgcag agaaatgccc cattgttatt tattccccag tgactccagg      1567
147 gtgacaa                                                              1574
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 391
152 <212> TYPE: PRT
153 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 2
156 Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala
157   1               5                   10                  15
158 Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
159             20                  25                  30
160 Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
161         35                  40                  45
162 Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
163     50                  55                  60
164 Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
165   65                70                  75                  80
166 Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
167             85                  90                  95
168 Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
169             100                 105                 110
170 Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
171         115                 120                 125
172 Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
173     130                 135                 140
174 Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
175 145                 150                 155                 160
176 Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
177             165                 170                 175
178 Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
179         180                 185                 190
180 Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
181         195                 200                 205
182 Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
183     210                 215                 220
184 Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
185 225                 230                 235                 240
186 Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
187             245                 250                 255
188 Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
```

```
189
190  Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
191       275                280                 285
192  Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
193       290            295               300
194  Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
195  305            310              315                 320
196  Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
197            325               330                335
198  Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
199       340             345               350
200  Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
201       355            360               365
202  Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
203       370            375               380
204  Leu Gly Glu Ala Pro Ala Ser
205  385               390
209  <210> SEQ ID NO: 3
210  <211> LENGTH: 1661
211  <212> TYPE: DNA
212  <213> ORGANISM: Mus musculus
214  <220> FEATURE:
215  <221> NAME/KEY: CDS
216  <222> LOCATION: (142)..(1275)
218  <400> SEQUENCE: 3
219  tcaggaacgg gtccctgcag cccccagccg atggcaggac agtagtcgcc tgtcaggggt 60
221  cgtgaaggac tgaggcagag gcagaggctc ccggagaggc agaggctccc gggcctcaga 120
223  tagtggttgt ctctggaggc c atg ggc tac cca gag gta gag cgc agg gaa  171
224                         Met Gly Tyr Pro Glu Val Glu Arg Arg Glu
225                          1               5                 10
227  ccc ctg cct gcg gca gcg cca agg gag cgg ggc agc cag ggc tgc ggc  219
228  Pro Leu Pro Ala Ala Ala Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly
229                15              20                25
231  tgt cgc ggg gcc cct gct cgg gcg ggc gaa ggg aac agc tgc cgg ctc  267
232  Cys Arg Gly Ala Pro Ala Arg Ala Gly Glu Gly Asn Ser Cys Arg Leu
233            30              35              40
235  ttc ctg ggt ttc ttt ggc ctc tcg ctg gcc ctc cac ctg ctg acg ctg  315
236  Phe Leu Gly Phe Phe Gly Leu Ser Leu Ala Leu His Leu Leu Thr Leu
237            45              50              55
239  tgc tgc tac cta gag ttg cgg tcc gaa ttg cgg cgg gaa cgg gga acc  363
240  Cys Cys Tyr Leu Glu Leu Arg Ser Glu Leu Arg Arg Glu Arg Gly Thr
241       60              65              70
243  gag tcc cgc ctc ggt ggc ccg ggt gct cct ggc acc tct ggc acc cta  411
244  Glu Ser Arg Leu Gly Gly Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu
245  75              80              85                 90
247  agc agc cct ggg agc ctc gac ccg gtg ggt ccc atc acc cgc cac ctg  459
248  Ser Ser Pro Gly Ser Leu Asp Pro Val Gly Pro Ile Thr Arg His Leu
249            95              100               105
251  ggg cag ccg tcc ttt caa cag cag cct ttg gaa ccg gga gaa gat cca  507
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/729,658C

DATE: 08/06/2002
TIME: 17:02:16

Input Set : A:\55924.app
Output Set: N:\CRF3\08062002\I729658C.raw

```
252 Gly Gln Pro Ser Phe Gln Gln Gln Pro Leu Glu Pro Gly Glu Asp Pro
253          110              115              120
255 ctc ccc cct gag tcc cag gac cgg cac cag atg gcc ctc ctg aat ttc   555
256 Leu Pro Pro Glu Ser Gln Asp Arg His Gln Met Ala Leu Leu Asn Phe
257          125              130              135
259 ttc ttt cct gat gaa aag gca tat tct gaa gag gaa agt agg cgt gtt   603
260 Phe Phe Pro Asp Glu Lys Ala Tyr Ser Glu Glu Glu Ser Arg Arg Val
261          140              145              150
263 cgc cgc aat aag aga agc aaa agt ggt gaa gga gca gat ggt cct gtt   651
264 Arg Arg Asn Lys Arg Ser Lys Ser Gly Glu Gly Ala Asp Gly Pro Val
265 155              160              165              170
267 aaa aac aag aaa aag gga aag aag gca ggg cca cct ggg ccc aac ggc   699
268 Lys Asn Lys Lys Lys Gly Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly
269              175              180              185
271 ccc cca gga cct cca gga cct ccg gga ccc cag gga cct cca ggg att   747
272 Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile
273              190              195              200
275 cca gga att cct ggg att cca gga aca act gtt atg gga cca cct ggc   795
276 Pro Gly Ile Pro Gly Ile Pro Gly Thr Thr Val Met Gly Pro Pro Gly
277          205              210              215
279 cca cct ggc cct cct ggt cct caa gga ccc cct ggc ctc caa gga cct   843
280 Pro Pro Gly Pro Pro Gly Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro
281          220              225              230
283 tct ggt gct gct gat aaa act gga act cgg gaa aat cag cca gct gtg   891
284 Ser Gly Ala Ala Asp Lys Thr Gly Thr Arg Glu Asn Gln Pro Ala Val
285 235              240              245              250
287 gtg cat ctg cag ggc caa ggg tca gca att caa gtc aaa aat gat ctt   939
288 Val His Leu Gln Gly Gln Gly Ser Ala Ile Gln Val Lys Asn Asp Leu
289              255              260              265
291 tca ggt gga gtg ctc aat gac tgg tct cgc atc act atg aac cct aag   987
292 Ser Gly Gly Val Leu Asn Asp Trp Ser Arg Ile Thr Met Asn Pro Lys
293              270              275              280
295 gtg ttt aaa cta cat ccc cgc agc ggg gag ctg gag gtc tac tac atc   1035
296 Val Phe Lys Leu His Pro Arg Ser Gly Glu Leu Glu Val Tyr Tyr Ile
297          285              290              295
299 aac ttc act gac ttt gcc agc tac gag gtg gtg gtg gat gag aag ccc   1083
300 Asn Phe Thr Asp Phe Ala Ser Tyr Glu Val Val Val Asp Glu Lys Pro
301          300              305              310
303 ttc ctg cag tgc acc cgc agc att gag aca ggg aag acc aac tac aac   1131
304 Phe Leu Gln Cys Thr Arg Ser Ile Glu Thr Gly Lys Thr Asn Tyr Asn
305 315              320              325              330
307 act tgc tat act gca ggc gtg tgc ctc ctc aag gcc agg cag aaa atc   1179
308 Thr Cys Tyr Thr Ala Gly Val Cys Leu Leu Lys Ala Arg Gln Lys Ile
309          335              340              345
311 gcc gtg aag atg gtg cac gct gac atc tct atc aat atg agc aag cac   1227
312 Ala Val Lys Met Val His Ala Asp Ile Ser Ile Asn Met Ser Lys His
313          350              355              360
315 acc acc ttc ttc ggg gcc atc agg ctg ggc gaa gcc cct gca tcc tag   1275
316 Thr Thr Phe Phe Gly Ala Ile Arg Leu Gly Glu Ala Pro Ala Ser
```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/729,658C

DATE: 08/06/2002
TIME: 17:02:17

Input Set : A:\55924.app
Output Set: N:\CRF3\08062002\I729658C.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 65
Seq#:9; N Pos. 754
Seq#:11; N Pos. 302
Seq#:12; N Pos. 2961,3423,3673
Seq#:43; N Pos. 39
Seq#:95; N Pos. 133,168,212,239,280,427,428,429
Seq#:97; N Pos. 453,533,579
Seq#:101; N Pos. 330,331,337,357,368,379,380,383,394,395,398,401,417,419
Seq#:101; N Pos. 423,434,435,436,442,443,447,448,450,452,454,457,460,462
Seq#:101; N Pos. 463,467,469,470,485,486,489,492,494,499,504,508,509,511
Seq#:101; N Pos. 518,522,534,537,542,544,545,559,572,574,586,597,602,603
Seq#:101; N Pos. 607,615,623,627,629,631,638,641,642,651,664,665,668,669
Seq#:101; N Pos. 673,690,695,697,706,717,718,719,731,742,743,753,757,760
Seq#:101; N Pos. 767,806,815,832,839,871,1163
Seq#:103; N Pos. 300,307
Seq#:105; N Pos. 325,397,400,403,416,433,441,454,460,462,474,479,487,495
Seq#:105; N Pos. 497,499,519,549,555,574,642
Seq#:109; N Pos. 190
Seq#:111; N Pos. 64,473,489,583,604,613,625,627,632,637,640,679,699,717,752
Seq#:112; N Pos. 19
Seq#:113; N Pos. 210,213,219,222,225
Seq#:115; N Pos. 8,9,16,26,37,41,54,60,61,62,83,88,92,95,98,100,102,105,109
Seq#:115; N Pos. 114,117,123,131,139,141,144,148,154,155,157,165,171,177
Seq#:115; N Pos. 185,187,188,189,193,202,204
Seq#:116; N Pos. 528,626,665,2141,2665,2721,2722,2756